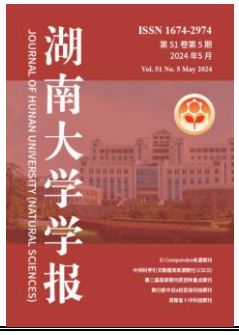

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The Multi-Step Adomian Decomposition Method Applied to an SEIR COVID-19 Mathematical Model with a Vaccinated Population

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Abstract: This paper presents a novel multistep approach with a new criterion to enhance the convergence interval of the Adomian decomposition method (ADM). The objective of this research was to apply the multi-step ADM to obtain an analytical solution for a mathematical model of the SEIR COVID-19 outbreak that includes partially and fully vaccinated individuals. The accuracy and efficiency of this method are demonstrated through a comparison with the existing literature. Moreover, this analytical-numerical approach was employed to generate and analyze vaccination strategy scenarios under various conditions and model parameters.

Keywords: SEIR COVID-19 mathematical model, the Adomian decomposition method, multi-step methodology, simulation, vaccinated population.

多步阿多米安分解法应用于具有疫苗接种人群的新冠肺炎疫情数学模型

摘要：本文提出了一种新颖的多步方法，并提出了一种新标准来增强阿多米安分解方法(腺苷二磷酸)的收敛区间。本研究的目的是应用多步腺苷二磷酸来获得新冠肺炎疫情疫情数学模型的解析解，该模型包括部分和完全接种疫苗的个体。通过与现有文献的比较证明了该方法的准确性和效率。此外，还采用了这种解析数值方法来生成和分析各种条件和模型参数下的疫苗接种策略方案。

关键词：新冠肺炎疫情数学模型、阿多米安分解方法、多步骤方法、模拟、接种疫苗人群。

1. Introduction

The COVID-19 pandemic was an unexpected event that exposed the world's vulnerability and impacted individuals and families indiscriminately; work, academic, and daily life activities were strongly affected [1-4]. During past pandemics such as AH1N1 influenza, SARS, MERS, and Zika, the scientific community implemented various prevention measures to impede contagion and contain the spread of the outbreak [5-10]. Various strategies have been implemented worldwide to decrease the transmission of this illness. Monitoring at both local and global levels has enabled us to track the progress of COVID-19 at all social, academic, and economic levels [3, 11]. In

developed nations, contagion has spread because of high levels of interaction between people of different social status [11, 12]. However, the implemented strategies have proven effective, as demonstrated by Iceland, a country with a population of less than a million people, which was considered the first country to successfully eradicate COVID-19 in 2020 [13]. Sanitary measures were instrumental in controlling the epidemic, and quarantining immigrants effectively prevented the spread of the disease among residents [2, 11, 13]. The epidemic has intensified in underdeveloped nations because of inadequate measures for preventing transmission. Studies have been conducted globally to identify vaccine types capable of reducing transmission among the population [14]. Collaboration between health institutions has increased scientific innovation in vaccine development. Some of the most notable vaccines are the Pfizer-BioNTech vaccine, which boasts a 90% effectiveness rate, the Russian Sputnik V vaccine with a 92% effectiveness rate, the AstraZeneca-Oxford University vaccine with a 70% effectiveness rate, and the Moderna vaccine with a 94% effectiveness rate [14-16]. It is important to note the efficacy rates of each vaccine, which helps in the implementation of sanitary measures to control the disease [17, 18].

One approach to studying epidemic behavior is to analyze a mathematical model that depicts disease evolution at both the virus and population levels. Since the emergence of COVID-19, researchers have endeavored to comprehend the disease's transmission mechanism through models expressed using ordinary differential equations, such as the SIR and SEIR models [11, 19]. Objective analyses of collected data can be used to assess the efficacy of various preventive measures, including social distancing and vaccination [12, 19]. More sophisticated models have been created to examine hospital requirements, the impact of vaccination interventions against the disease, and the outcomes of early school leaving at specific educational levels [3, 18, 20]. One must develop solution strategies to create mathematical models by employing traditional methods like Runge-Kuta, Euler, and others [21]. Probabilistic methods such as Bayesian or Monte Carlo methods have been employed to estimate the uncertainty in the spread of the COVID-19 disease in [11, 22].

In the 1980s, George Adomian developed the Adomian decomposition method (ADM), an effective approach for solving differential equations [23]. The versatility of this approach has led to its widespread application across various disciplines such as chemistry, biology, engineering, and physics. It provides analytic solutions for a wide range of differential equations including ordinary, partial, deterministic, stochastic, and delayed equations. This has made a significant impact in advancing scientific research across multiple fields [24-27].

This paper applies the ADM to solve a SEIR mathematical model with a vaccinated population for the analysis of the COVID-19 outbreak. We contrast the approximations with the ADM with the solutions obtained through the fourth-order Runge-Kutta, which can be found in the literature [21]. A multi-step methodology was used to enhance the convergence interval of the analytical solution series. This study demonstrated the feasibility of the proposed approach by simulating possible COVID-19 vaccination scenarios.

2. SEIR COVID-19 Mathematical Model

We consider the mathematical model presented in [21], which incorporates the effects of partially and fully vaccinated individuals.

This model decomposes the population $n(t)$ into subpopulations: the susceptible population $S(t)$, the exposed population $E(t)$, the infected population $I(t)$, and the recovered population $R(t)$, satisfying $n(t) = S(t) + E(t) + I(t) + R(t)$.

The mathematical model, which is defined by a set of differential equations, is then presented as follows

$$\begin{cases} \frac{dS}{dt} = A - \alpha S I - \mu S - V_p S - V_f S, \\ \frac{dE}{dt} = \alpha S I - \mu E - \delta E + V_p S, \\ \frac{dI}{dt} = \delta E - \mu I - \mu_1 I - \gamma I, \\ \frac{dR}{dt} = V_f S + \gamma I - \mu R \end{cases} \tag{1}$$

where A represents the recruitment rate, α indicates the rate of interaction between the susceptible and infected populations, μ is the death rate; V_p and V_f represent the partially and fully vaccinated populations, respectively; $\delta > 0$ denotes the rate at which the exposed population becomes infected, μ_1 represents the disease-related rate, and γ is the rate of medication recovery.

3. Description of the ADM

The ADM is used to obtain a series solution by decomposing the differential operator into three main components: the linear operator L, the non-linear operator N, and the independent function g. The operator L is decomposed into $L + R$, where L is the highest-order linear operator and R is the remaining linear operator. The ADM uses the inverse of the higher-order linear differential operator, L^{-1}, applied to the entire differential equation or system. In this process, the initial and boundary conditions are included. The nonlinear P term of the equation is decomposed into a sum of polynomials as $\sum_{n=0}^{\infty} A_n$, where the A_n are called the Adomian polynomials and depend on the non-linearity of N. Multiple formulas can be used to generate these polynomials. A practical method for calculating Adomian polynomials was also introduced in [28]. Finally, the solution is considered a sequence of terms that are recursively calculated. The ADM is described as follows:

Let us consider a general system with m nonlinear

differential equations:

$$\begin{cases} L_1u_1 + R_1(u_1, u_2, ..., u_m) + N_1(u_1, u_2, ..., u_m) = g_1, \\ L_2u_2 + R_2(u_1, u_2, ..., u_m) + N_2(u_1, u_2, ..., u_m) = g_2, \\ \vdots \\ L_mu_m + R_m(u_1, u_2, ..., u_m) + N_n(u_1, u_2, ..., u_m) = g_m, \end{cases} \quad (2)$$

where L_i is the highest-order linear operator of L, R_i is the remainder of the linear operator of L, N_i is the nonlinear operator, and g_i is the independent function for the *i*-th equation of the system for *i = 1, ..., m*.

Let $U = (u_1, u_2, \ldots, u_m)$ be given and apply the inverse operator L_i^{-1} to its corresponding equation (2):

$$\begin{cases} u_1 = \Phi_1 + L_1^{-1}g_1 - L_1^{-1}R_1(\mathcal{U}) - L_1^{-1}N_1(\mathcal{U}), \\ u_2 = \Phi_2 + L_2^{-1}g_2 - L_2^{-1}R_2(\mathcal{U}) - L_2^{-1}N_2(\mathcal{U}), \\ \vdots \\ u_m = \Phi_m + L_m^{-1}g_m - L_m^{-1}R_m(\mathcal{U}) - L_m^{-1}N_m(\mathcal{U}), \end{cases} \quad (3)$$

where Φ_i includes all the initial conditions necessary to solve the initial value problem [26] for *i = 1, ..., m*. Let us assume that the state variables are decomposed as follows:

$$\mathcal{U} = \sum_{n=0}^{\infty} \mathcal{U}_n, \quad (4)$$

where $U_j = (u_{1,j}, u_{2,j}, \ldots, u_{m,j})$ for *j = 0,..., n*, i.e., $u_i = \sum_{n=0}^{\infty} u_{i,n}$ for *i = 1,..., m*. The nonlinear term of each equation is decomposed into a series of Adomian polynomials:

$$N_i(\mathcal{U}) = \sum_{n=0}^{\infty} A_{i,n}(\mathcal{U}_0, \mathcal{U}_1, \ldots, \mathcal{U}_n), \quad (5)$$

and

$$A_{i,n}(\mathcal{U}_0, \mathcal{U}_1, \ldots, \mathcal{U}_n) = \frac{1}{n!}\frac{d^n}{d\lambda^n}\left[N_i\left(\sum_{j=0}^{\infty}\lambda^j u_{1,j}, \sum_{j=0}^{\infty}\lambda^j u_{2,j}, .. \sum_{j=0}^{\infty}\lambda^j u_{m,j}\right)\right]_{\lambda=0}, \quad (6)$$

for *i = 1, 2, ...m*. Several convenient algorithms and efficient subroutines for quickly generating Adomian polynomials have been reported [28, 29]. The solution to the problem presented by system (2) is as follows:

$$\begin{cases} u_1 = \sum_{n=0}^{\infty} u_{1,n} = \Phi_1 - L_1^{-1}g_1 - L_1^{-1}\sum_{n=0}^{\infty} R_1(\mathcal{U}) \\ \qquad -L_1^{-1}\sum_{n=0}^{\infty} A_{1,n}(\mathcal{U}_0, \mathcal{U}_1, \ldots, \mathcal{U}_n) \\ u_2 = \sum_{n=0}^{\infty} u_{2,n} = \Phi_2 - L_2^{-1}g_2 - L_2^{-1}\sum_{n=0}^{\infty} R_2(\mathcal{U}) \\ \qquad -L_2^{-1}\sum_{n=0}^{\infty} A_{2,n}(\mathcal{U}_0, \mathcal{U}_1, \ldots, \mathcal{U}_n) \\ \vdots \\ u_m = \sum_{n=0}^{\infty} u_{m,n} = \Phi_n - L_m^{-1}g_m - L_m^{-1}\sum_{n=0}^{\infty} R_m(\mathcal{U}) \\ \qquad -L_m^{-1}\sum_{n=0}^{\infty} A_{m,n}(\mathcal{U}_0, \mathcal{U}_1, \ldots, \mathcal{U}_n) \end{cases} \quad (7)$$

Then, the terms of series (4) can be expressed as follows:

$$\begin{cases} u_{i,0} = \Phi_i + L^{-1}g_i \ , \\ u_{i,n+1} = -L_i^{-1}R_i(\mathcal{U}_n) - L_i^{-1}A_{i,n}(\mathcal{U}_0, \mathcal{U}_1, \ldots, \mathcal{U}_n), \\ \phi_{i,n+1} = \sum_{j=0}^{n} u_{i,j} \ , \quad n \geq 0 \end{cases} \quad (8)$$

The series in expression (8) generally converge very rapidly in real physical problems, which means that few terms are required for the approximation. In the literature, necessary conditions, analysis, and results regarding the convergence of series to the exact solution for expression (4) are reported in [23, 30], and the limit of the series satisfies

$$\lim_{j\to\infty} \phi_{i,j} = u_i, \text{ for } i = 1, ..., m \quad (9)$$

Similarly to a power series expansion or a Taylor expansion series, the Adomian decomposition series may have a convergence interval that is smaller than that required for solution analysis. In other words, the method typically results in a local solution rather than a global one; the approximate analytic solution is close to the exact solution only as *t* approaches the initial time t_0. For large *t* values, the solution deviates from the exact solution [31]. However, references to algorithms capable of obtaining a solution within any arbitrary interval $[t_0, T]$ are cited in [25, 31, 32]. Other proposals include adaptations of the diagonal Padé approximants [33] or multistage techniques [34, 35].

4. Application to the COVID-19 Model

In this section, we apply the ADM algorithm to the SEIR model presented in Section 2. The highest order of the linear differential operator in the mathematical model is $\frac{d(*)}{dt}$; then, we rewrite system (1) considering $L^{-1} = \int_0^t (*)dt$:

$$\begin{cases} S(t) = S(0) + At - (\mu + V_p + V_f)\int_0^t S(t)dt - \alpha\int_0^t S(t)I(t)dt, \\ E(t) = E(0) + \alpha\int_0^t S(t)I(t)dt - (\mu + \delta)\int_0^t E(t)dt + V_p\int_0^t S(t)dt, \\ I(t) = I(0) + \delta\int_0^t E(t)dt - (\mu + \mu_1 + \gamma)\int_0^t I(t)dt - \mu_1 I - \gamma I, \\ R(t) = R(0) + V_f\int_0^t S(t)dt + \gamma\int_0^t I(t)dt - \mu\int_0^t R(t)dt \end{cases} \quad (10)$$

We now consider the decomposition of $S(t), E(t), I(t), R(t)$ as a series:

$$S(t) = \sum_{n=0}^{\infty} S_n(t), \quad E(t) = \sum_{n=0}^{\infty} E_n(t), \quad I(t) = \sum_{n=0}^{\infty} I_n(t), \quad R(t) = \sum_{n=0}^{\infty} I_n(t), \quad (11)$$

The nonlinear term is decomposed as

$$S(t)I(t) = \sum_{n=0}^{\infty} A_n(t), \quad (12)$$

where $A_n(t)$ is the *n*-th Adomian polynomial described by Eq. (5) and (6).

Then, we obtain

$$\begin{cases} \sum_{n=0}^{\infty} S_n(t) = S(0) + At - (\mu + V_p + V_f)\int_0^t \sum_{n=0}^{\infty} S_n(t)dt \\ \qquad - \alpha\int_0^t \sum_{n=0}^{\infty} A_n(t)dt, \\ \sum_{n=0}^{\infty} E_n(t) = E(0) + \alpha\int_0^t \sum_{n=0}^{\infty} A_n(t)dt \\ \qquad - (\mu + \delta)\int_0^t \sum_{n=0}^{\infty} E_n(t)dt + V_p\int_0^t \sum_{n=0}^{\infty} S_n(t)dt, \\ \sum_{n=0}^{\infty} I_n(t) = I(0) + \delta\int_0^t \sum_{n=0}^{\infty} E_n(t)dt \\ \qquad - (\mu + \mu_1 + \gamma)\int_0^t \sum_{n=0}^{\infty} I_n(t)dt, \\ \sum_{n=0}^{\infty} R_n(t) = R(0) + V_f\int_0^t \sum_{n=0}^{\infty} S_n(t)dt + \gamma\int_0^t \sum_{n=0}^{\infty} I_n(t)dt \\ \qquad - \mu\int_0^t \sum_{n=0}^{\infty} R_n(t)dt \end{cases} \quad (13)$$

By examining the series with k > 0 terms, we can identify the individual terms and derive the following recursive expression:

$$\begin{cases} S_0(t) = S(0) + At, \\ E_0(t) = E(0), \\ I_0(t) = I(0), \\ R_0(t) = R(0), \end{cases}$$

$$\begin{cases} S_{k+1}(t) = -(\mu + V_p + V_f)\int_0^t S_k(t)dt - \alpha\int_0^t A_k(t)dt, \\ E_{k+1}(t) = \alpha\int_0^t A_k(t)dt - (\mu+\delta)\int_0^t E_k(t)dt + V_p\int_0^t S_k(t)dt, \\ I_{k+1}(t) = \delta\int_0^t E_k(t)dt - (\mu+\mu_1+\gamma)\int_0^t I_k(t)dt, \\ R_{k+1}(t) = V_f\int_0^t S_k(t)dt + \gamma\int_0^t I_k(t)dt - \mu\int_0^t R_k(t)dt \end{cases} \quad (14)$$

In this paper, an algorithm to increase the solution interval of the ADM is proposed. The algorithm solves the system with the initial condition $\phi_0 = [S(0), E(0), I(0), R(0)]$ at time t_0, considers time step size Δt, and evaluates the solution at time $t_{i+1} = t_i + \Delta t$ for $i > 0$. If the evaluation of t_{i+1} in the solution is such that $max\{\phi(t_{i+1})\} > \epsilon$ for a fixed $\epsilon > 0$, Δt is discarded, and the ADM is restarted with $\phi_0 = \phi(t_i)$ as the initial condition at t_i (Algorithm 1 in Fig. 1).

Algorithm 1 Adomian decomposition method for SEIR COVID-19 model Algorithm

Step 1. Input: Set
Initial conditions $t_0, S(0), E(0), I(0), R(0)$,
Number of terms of the series approximation n,
Tolerance ε,
Maximum time T,
Number of discretizations N of T,
Linear terms R, non-linear terms N, and independent terms g,
$[[S_R, S_N, S_g], [E_R, E_N, E_g], [I_R, I_N, I_g], [R_R, R_N, R_g]]$
Set $i = 0$, $t_i = t_0$, $band = 0$. and $\Delta_t = T/N$.
Step 2.
$band = band + 1$,
Obtain the solution using the ADM with initial condition at t_0,

$$\vec{\Phi} = \sum_{j=0}^{n-1} \vec{\phi}_j,$$

where $\vec{\phi} = (S, E, I, R)$.
Step 3.
while $i < N$ **do**
  $t_{i+1} = t_i + \Delta_t$
  if $max\{\phi_{n-1}^h(t_{i+1})\}_h < \varepsilon$, for $h = \{S, E, I, R\}$ **then**
    Go to step 3.
  else
    if $band = 1$ **then**
      $T_1 = t_i$
      Output: approximation of the system on $[T_0, T_1]$
      $T_0 = t_i$
      Go to step 2.
    else
      $band = 1$
      Go to step 3.
    end if
  end if
end while
Step 4.
if $T_1 \neq T$ **then**
  Output: $\vec{\Phi}_n(t)$ on $[T_0, T]$
end if

Fig. 1 Algorithm for the ADM (The author)

5. Results and Discussion

This section presents the solution of system (1) for the COVID-19 model with vaccination using the ADM, which is compared with the result obtained in [21]. The ADM algorithm is coded in Maple Software [26, 27]. For the implementation of Algorithm 1 in this paper, a fixed value of tolerance is set as $\epsilon = 1 \times 10^{-5}$.

To compare the results of the ADM, we examine Base Case 1. This case involves utilizing the parameters outlined in Table 1 for the SEIR COVID-19 model with a vaccinated population. These values were reported in [21]. This parameter list was applied to describe COVID-19 in the capital of Kerala, Trivandrum. The authors used the fourth-order Runge-Kutta and Euler methods to solve the set of differential equations. On the zero day of the simulation, in [21], there were 1,679,754 individuals in the population. Of these, 1,661,989 were considered susceptible, 1,661 were exposed, 481 were infected, and 487 had recovered.

Table 1 Parameters presented in [21]

A	α	μ	V_p	V_f	δ	μ_1	γ
33,595	1e−5	0.143	0.2522	0.1517	1.01	0.1595	0.9

Fig. 2 compares the results obtained using the ADM and fourth-order Runge-Kutta methods over 35 days. In Fig. 2a and b, the solutions are very similar in both methods, and in Fig. 2c and d, the analytical solution demonstrates a variation in the results while maintaining the maximum peak. Overall, the profiles exhibit similarities and offer insight into the progression of the COVID-19 outbreak.

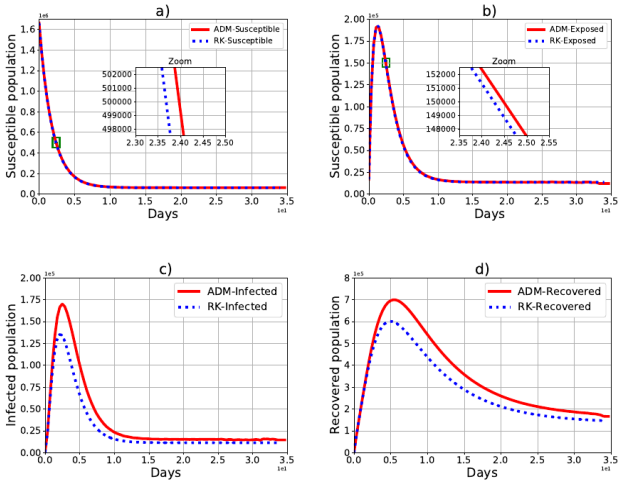

Fig. 2 Results of the ADM compared with the fourth-order Runge-Kutta (RK) method (The author)

5.1. Simulations of Partial and Full Vaccination

Using the ADM, let us consider the cases where the types of vaccination in a population change. Let us consider two scenarios. In the first scenario, the population has been promptly attended to with health restrictions, social distancing measures being

maintained, and everyone has completed their vaccination schedule. In the second scenario, due to limitations, the population is still undergoing partial vaccination.

Let us define "ADM-full vaccination" as a scenario in which the population has completed their full vaccination schedule. Then, the parameter for partial vaccination is set as $V_p = 0$. On the other hand, let us refer to "ADM-partial vaccination" as a scenario in which the population has received some, but not full, vaccination; then, $V_f = 0$. The remaining parameters of the mathematical model are identical to those of the base case (ADM-Base Case 1) (Table 1).

Fig. 3 shows the evolution of the subpopulations over 35 days of the pandemic. For the ADM-partial vaccination case, the impact of partial vaccination implies that the exposed population increases by ≈ 24,330 people compared to the ADM-Base Case 1 (partial vaccination + full vaccination schedule), while for the total vaccination case, the exposure is much lower because people already have defenses and remain susceptible (Fig. 3a and b).

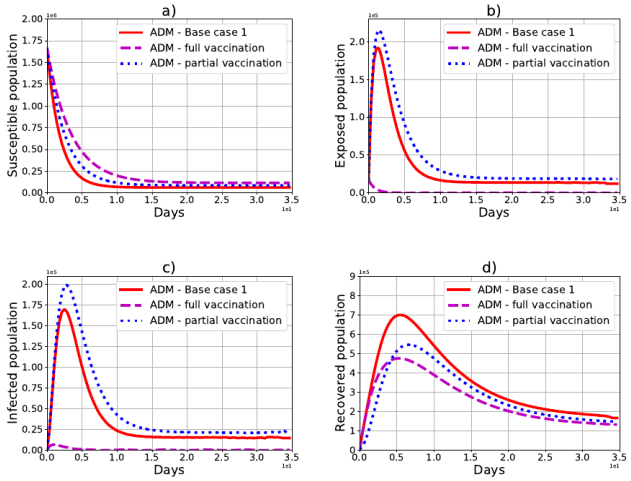

Fig. 3 Results of the ADM after 35 days for different vaccination cases (The author)

In comparison to the ADM-Base Case 1, the number of infected individuals increases by around ≈ 29,300 in the case of partial vaccination and decreases by ≈ 163,500 individuals in the case of the full vaccination schedule (Fig. 3c). The number of people who recover is lower in the case of total vaccination because there are fewer infected people (Fig. 3d).

5.2. Methodology Robustness: Fictitious Scenario with Vaccination

The robustness of the ADM using the proposed methodology is demonstrated by varying the parameter values of the model. Table 2 presents the set of parameters, whereas the initial values for the differential equation system remain consistent with the previous scenarios in Section 5.1.

Table 2 Parameters for Scenario 2 (The author)

A	α	μ	V_p	V_f	δ	μ_1	γ
33,595	0.9	0.043	0.2522	0.1517	2.0	0.1595	0.5

In this case, we consider extreme but possibly realistic scenarios. We assume that the rate of interaction between the susceptible population and the infected population is heightened, indicating increased contact between these two subpopulations. This phenomenon mirrors real-life scenarios where individuals are inevitably concentrated due to commuting on public transportation, attending schools or workplaces, visiting crowded areas, and being in confined or cramped spaces. Additionally, these interactions occur in places with minimal sanitary measures and potentially no social distancing protocols in place. Thus, individuals may be at an increased risk of contracting infectious diseases. The parameter γ is decremented due to low medication access, which may be attributed to economic challenges, remote locations, or medication shortages. The parameter μ is decremented because mortality is lower in young people than in older people; finally, δ increases due to the exposure increases.

With the previous assumptions, let us consider the scenarios using the set of parameters in Table 2, the ADM-Base Case 2 with partial and complete vaccination ($V_p \neq 0, V_f \neq 0$), the ADM-full vaccination case in which the whole population has been vaccinated ($V_p = 0$), and the ADM-partial vaccination case in which the population has only a partial vaccination schedule ($V_f = 0$).

The simulation results are displayed in Fig. 4. In comparison with the base case (ADM-Base Case 2), the susceptible population is greater for the full vaccination case (Fig. 4a), whereas the exposed population is lower (Fig. 4b). As a result, the number of infections is also lower (Fig. 4c), and those who recover are expected to increase compared to the case of partial vaccination (Fig. 4d). This is attributed to the complete vaccination schedule, which provides individuals with better defense against the virus.

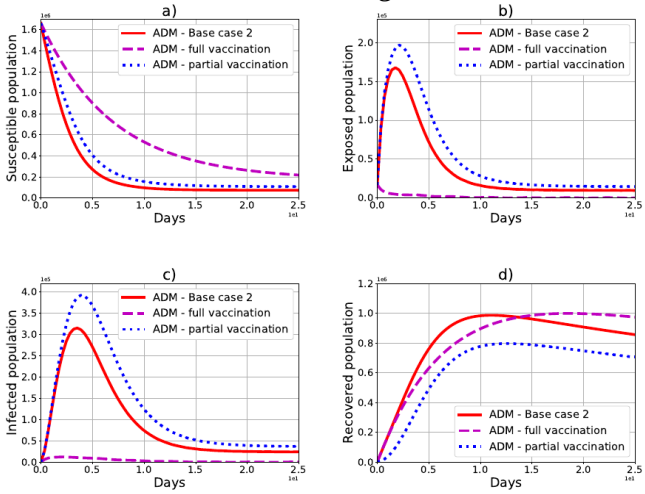

Fig. 4 Comparative ADM results under different extreme parameters (The author)

With partial vaccination (ADM-partial vaccination), there is a quicker decrease in the number of susceptible individuals compared to the full vaccination case (Fig. 4a). This is due to greater exposure to the virus and faster infection rates resulting from interactions with infected individuals. Incomplete vaccination schedules also resulted in lower recovery rates (Fig. 4d).

Based on the obtained results, the proposed methodology continues to replicate the expected behavior of the state variables in the model, thereby allowing new scenarios to be explored under extreme conditions.

6. Conclusion

This paper presents the application of the ADM to provide an analytical solution for a mathematical model of the SEIR COVID-19 outbreak in a partially and fully vaccinated population. The multi-step ADM algorithm (Algorithm 1) is proposed to increase the convergence interval of the analytic solution series in the mathematical model analyzed in this research. The results are consistent with findings in the literature, indicating that the ADM is a dependable alternative for addressing this significant model. This study introduces modifications to the SEIR model by setting $V_f = 0$ and $V_p = 0$ to analyze the influence of partially and fully vaccinated populations on the epidemic dynamics.

This research introduces a novel method for solving systems of differential equations with initial conditions over extended time intervals using the ADM. The main contribution of this research is the development of a methodology that can enhance the convergence interval in the ADM. This methodology can be adapted to other analytical methods used to solve differential equations in series expansion. For example, Algorithm 1 can be adapted in conjunction with methods derived from the variational iteration method.

In future research, we will explore new criteria aimed at enhancing the convergence interval of the ADM. These criteria will be tested and implemented in other expansion series methods to effectively address ODEs within epidemic models. Specifically, we will consider models with more intricate assumptions such as virus mutations. Our goal is to investigate the dynamics of these variants and their implications for public health measures within the population.

In the field of healthcare, conducting studies using this methodology enables the acquisition of analytical solutions and the exploration of various scenarios. These are crucial for making informed decisions in managing a pandemic at a regional or national level.

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